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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/759,463

DATE: 08/30/2004

TIME: 14:42:30

Input Set : N:\Crf3\RULE60\10759463.raw.txt

Output Set: N:\CRF4\08302004\J759463.raw

1 <110> APPLICANT: Itadani, Hiraku
 2 Takimura, Tetsuo
 3 Nakamura, Takao
 4 Kobayashi, Masahiko
 5 Tanaka, Ken-ichi
 6 Hidaka, Yusuke
 7 Ohta, Masataka
 8 <120> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
 9 BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
 10 <130> FILE REFERENCE: 06501-083001
 11 <140> CURRENT APPLICATION NUMBER: US/10/759,463
 12 <141> CURRENT FILING DATE: 2004-01-16
 13 <150> PRIOR APPLICATION NUMBER: US/09/891,053
 14 <151> PRIOR FILING DATE: 2001-06-25
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/07280
 16 <151> PRIOR FILING DATE: 1999-12-24
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/05967
 18 <151> PRIOR FILING DATE: 1998-12-25
 19 <150> PRIOR APPLICATION NUMBER: JP 11/145661
 20 <151> PRIOR FILING DATE: 1999-05-25
 21 <160> NUMBER OF SEQ ID NOS: 26
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 413
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Rattus norvegicus
 28 <400> SEQUENCE: 1
 29 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 30 1 5 10 15
 31 Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 32 20 25 30
 33 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 34 35 40 45
 35 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 36 50 55 60
 37 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 38 65 70 75 80
 39 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 40 85 90 95
 41 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
 42 100 105 110
 43 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
 44 115 120 125

ENTERED

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45 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
46 130 135 140
47 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
48 145 150 155 160
49 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
50 165 170 175
51 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
52 180 185 190
53 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
54 195 200 205
55 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
56 210 215 220
57 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
58 225 230 235 240
59 Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
60 245 250 255
61 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
62 260 265 270
63 His Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
64 275 280 285
65 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
66 290 295 300
67 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
68 305 310 315 320
69 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
70 325 330 335
71 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
72 340 345 350
73 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
74 355 360 365
75 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
76 370 375 380
77 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
78 385 390 395 400
79 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
80 405 410
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 1239
84 <212> TYPE: DNA
85 <213> ORGANISM: Rattus norvegicus
86 <220> FEATURE:
87 <221> NAME/KEY: CDS
88 <222> LOCATION: (1)...(1239)
89 <400> SEQUENCE: 2
90 atg gag cgc ccc gac ggg ctg atg aac gcg tcg ggc act ctg 48
91 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
92 1 5 10 15
93 gcc gga gag gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 96
94 Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

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95	20	25	30	
96	tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca			144
97	Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr			
98	35	40	45	
99	gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc			192
100	Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser			
101	50	55	60	
102	ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac			240
103	Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp			
104	65	70	75	80
105	ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg			288
106	Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu			
107	85	90	95	
108	acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg			336
109	Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val			
110	100	105	110	
111	gta gac tac cta ctg tgt gcc tcc tgc gtc ttc aac atc gta ctc atc			384
112	Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile			
113	115	120	125	
114	agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc			432
115	Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala			
116	130	135	140	
117	cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg			480
118	Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp			
119	145	150	155	160
120	gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac			528
121	Val Leu Ala Phe Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr			
122	165	170	175	
123	ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc			576
124	Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe			
125	180	185	190	
126	ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc			624
127	Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe			
128	195	200	205	
129	acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac			672
130	Thr Pro Phe Leu Ser Val Thr Phe Asn Leu Ser Ile Tyr Leu Asn			
131	210	215	220	
132	atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc			720
133	Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly			
134	225	230	235	240
135	cca gaa ccc cca cca gat gcc cag ccc tgc cca cct cca gct ccc ccc			768
136	Pro Glu Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro			
137	245	250	255	
138	agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg			816
139	Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu			
140	260	265	270	
141	cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc			864
142	His Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu			
143	275	280	285	

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144	aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc	912
145	Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg	
146	290 295 300	
147	atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg	960
148	Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg	
149	305 310 315 320	
150	gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg	1008
151	Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly	
152	325 330 335	
153	ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc	1056
154	Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys	
155	340 345 350	
156	cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt	1104
157	His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu	
158	355 360 365	
159	ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac	1152
160	Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His	
161	370 375 380	
162	tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc	1200
163	Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu	
164	385 390 395 400	
165	aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag	1239
166	Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys	
167	405 410	

169 <210> SEQ ID NO: 3

170 <211> LENGTH: 21

171 <212> TYPE: DNA

172 <213> ORGANISM: Artificial Sequence

173 <220> FEATURE:

174 <223> OTHER INFORMATION: artificially synthesized primer sequence

W--> 175 <221> NAME/KEY: misc_feature

176 <222> LOCATION: (1)...(21)

177 <223> OTHER INFORMATION: n = A,T,C or G

W--> 178 <400> 3

W--> 179 batngccaaac ctbkccttct c 21

181 <210> SEQ ID NO: 4

182 <211> LENGTH: 20

183 <212> TYPE: DNA

184 <213> ORGANISM: Artificial Sequence

185 <220> FEATURE:

186 <223> OTHER INFORMATION: artificially synthesized primer sequence

W--> 187 <221> NAME/KEY: misc_feature

188 <222> LOCATION: (1)...(20)

189 <223> OTHER INFORMATION: n = A,T,C or G

W--> 190 <400> 4

W--> 191 ccataaaaagn nggggttgac 20

193 <210> SEQ ID NO: 5

194 <211> LENGTH: 2700

195 <212> TYPE: DNA

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196 <213> ORGANISM: Rattus norvegicus
 197 <220> FEATURE:
 198 <221> NAME/KEY: CDS
 199 <222> LOCATION: (351)...(1589)
 200 <221> NAME/KEY: misc_feature
 201 <222> LOCATION: (1)...(2700)
 202 <223> OTHER INFORMATION: n = A,T,C or G
 203 <400> 5
 204 aattcggcac gagcgggcag atcgcggggc gcactcggtt gcgcgctgag ctaggggtgc 60
 205 accgacgcac cgccggcggc tggagctcg cttgtctc gctgcagcag ccgcggccgc 120
 206 cgcggccactc cgctcagatt ccgacaccag cccctctgg atcgcctcc tggactctag 180
 207 cccgggctct tgctccgacc ccgcggacca tgctccggc gccccccgga aaaccgggct 240
 208 gggcgaagag ccggcaaaga ttaggctcac gagcgggggc cccacccggc caccagctc 300
 209 tccggccgtg ccctgcccgg tgcgtccgag ccgtgtgagc ctgctggcc atg gag 356
 210 Met Glu
 211 1
 212 cgc gcg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga 404
 213 Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly
 214 5 10 15
 215 gag gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc 452
 216 Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr
 217 20 25 30
 218 gct gtc ctg gct gca atg gcg ctg ctc atc gtg gcc aca gta ctg 500
 219 Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu
 220 35 40 45 50
 221 ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc 548
 222 Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg
 223 55 60 65
 224 acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc 596
 225 Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu
 226 70 75 80
 227 gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc 644
 228 Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly
 229 85 90 95
 230 cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac 692
 231 Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp
 232 100 105 110
 233 tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat 740
 234 Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr
 235 115 120 125 130
 236 gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag 788
 237 Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln
 238 135 140 145
 239 ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg 836
 240 Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu
 241 150 155 160
 242 gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct 884
 243 Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser
 244 165 170 175

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/759,463

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 4
Seq#:4; N Pos. 10,11
Seq#:5; N Pos. 2688
Seq#:11; N Pos. 20
Seq#:22; N Pos. 18
Seq#:23; N Pos. 18

VERIFICATION SUMMARY DATE: 08/30/2004
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Input Set : N:\Crf3\RULE60\10759463.raw.txt
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:178 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2629
L:365 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:679 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:682 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:691 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:694 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0